

MAY 0 1 2003

SEQUENCE LISTING

<110> Pfizer, Inc. and Pfizer Products, Inc.

<120> NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA HYOPNEUMONIAE mhp3  
GENE AND USES THEREOF

<130> 3153.00162/PC10555

<140> US 09/676,249

<141> 2000-09-29

<150> US Prov. 60/156,602

<151> 1999-09-29

<160> 42

<170> PatentIn version 3.2

<210> 1

<211> 1692

<212> DNA

<213> Mycoplasma hyopneumoniae

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aaagctgatg caaacaacaa ttttgggcta aatatggcaa ttgtaaccgc tgggtggaacg 360  
gtaaatgata attcatttaa ccaatcaagt tgagaggcaa ttcaacaact tggcgctctt 420  
actggagggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 480  
tcacttgcta ataccaacaa aaatgtttga gtactttctg gttttcaaca cggatgatgcg 540  
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atactcgga ttagactgaac tgatactgaa aatgtaattc caacaggctc atatattaat 660  
ttaacctata aaactgaaga agccggatga cttgcaggat atgcgaatgc ttcccttttg 720  
gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 780  
tcgccagctg taactgattt tatcgctggg tatctagccg gaattaaagc ttgaaatcta 840  
aaaaattctg ataaaaaac aaagataaca actgataaaa tcgagataaa tcttggggtt 900  
gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 960

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Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln Asn Lys Gln Ile  
35 40 45

Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu Arg Lys Ser Glu  
50 55 60

Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe Gly Leu Asn Met  
65 70 75 80

Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn Ser Phe Asn Gln  
85 90 95

Ser Ser Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu Thr Gly Gly Glu  
100 105 110

Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu Gly Lys Tyr Ser  
115 120 125

Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu Ser Gly Phe Gln  
130 135 140

His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro Glu Asn Lys Gln  
145 150 155 160

Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp  
165 170 175

Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn Leu Thr Tyr Lys  
180 185 190

Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn Ala Ser Phe Leu  
195 200 205

Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser Ala Ile Val Ile  
210 215 220

Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu  
225 230 235 240

Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp Lys Lys Thr Lys  
245 250 255

Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp  
260 265 270

Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro  
275 280 285

Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu Ile Phe Ser Asp  
290 295 300

Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly Val Asp Thr Asp  
305 310 315 320

Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe Phe Thr Ser Ile  
 325 330 335

Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu Ser Asp Leu Tyr  
 340 345 350

Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe Glu Phe Gly Lys  
 355 360 365

Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg Phe Val Asp Ile  
 370 375 380

Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu Ala Thr Glu Ala  
 385 390 395 400

Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr Lys Thr Ile Pro  
 405 410 415

Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu Met Pro Asp Lys  
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Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu Ile Thr Asp Ile  
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Asn Lys Asn  
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 aaagctgatg caaacaaca ttttgggcta aatatggcaa ttgtaaccgc tgggtggaacg 180  
 gtaaatagata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt 240  
 actggagggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 300  
 tcacttgcta ataccaacaa aaatgtttgg gtactttctg gttttcaaca cggtgatgag 360

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ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg 540
gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 600
tcgccagctg taactgattt tatcgctggg tatctagccg gaattaaagc ttggaatcta 660
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gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 780
tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac 840
caaatgatac gttatctcat tgggtgttgac accgaccaat cacttggtta tacaaaaact 900
aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 960
agtgatttat ataccaaaaa atcaaattca agaaatttag ccggctttga atttggtaaa 1020
aaaagtgcaa ccgtttatct tggaattaaa gacagggttg tcgatattgc tgatacttct 1080
ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt 1140
gaagaaaaaa ctaagacaat tctgcccga gaagtctgta aaactttaga aattccggaa 1200
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<210> 4
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<212> PRT
<213> Artificial Sequence

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<220>
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<222> (1)..(423)
<223> Xaa is any amino acid

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20          25          30

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Arg Lys Ser Glu Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe  
35 40 45

Gly Leu Asn Met Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn  
50 55 60

Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu  
65 70 75 80

Thr Gly Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu  
85 90 95

Gly Lys Tyr Ser Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu  
100 105 110

Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro  
115 120 125

Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile  
130 135 140

Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn  
145 150 155 160

Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn  
165 170 175

Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser  
180 185 190

Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile  
195 200 205

Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp  
210 215 220

Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe  
225 230 235 240

Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser  
245 250 255

Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu  
 260 265 270

Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly  
 275 280 285

Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe  
 290 295 300

Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu  
 305 310 315 320

Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe  
 325 330 335

Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg  
 340 345 350

Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu  
 355 360 365

Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr  
 370 375 380

Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu  
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Met Pro Asp Lys Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu  
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 gagctatatt ttccttcaag ttcagcagtt gaactatcta ctgaagtaat ctcacctcca 180

gtaagagcgc caagttgttg aattgcctct caacttgatt ggttaaata ga attatcattt 240  
 accgttccac cagcgggttac aattgccata tttagcccaa aatgtttgtt tgcacagct 300  
 tttgcggccca taatttcgga ttttcgttca ttaactagtc ctgaaatttt tgagacatca 360  
 gtgatttgct tattttgatt atcggctgat ttttcttctt tagttgtttc tttatcccaa 420  
 catccggcag agattgtcgc gattgctgaa agcggaaaaa ctaagcctaa gccaagaaat 480  
 ttatttcatt ttatcttttt tttcatagtt gttctcctaa ttaattgttt taattacgat 540  
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<210> 6  
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 <212> PRT  
 <213> *Mycoplasma hyopneumoniae*

<400> 6

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Asn His Leu Val Asn Ala Ser Pro Cys Trp Lys Pro Glu Ser Thr Gln  
 20 25 30

Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser  
 35 40 45

Ala Val Glu Leu Ser Thr Glu Val Ile Ser Pro Pro Val Arg Ala Pro  
 50 55 60

Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe  
 65 70 75 80

Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu  
 85 90 95

Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr  
 100 105 110

Ser Pro Glu Ile Phe Glu Thr Ser Val Ile Cys Leu Phe Trp Leu Ser  
 115 120 125

Ala Asp Phe Ser Ser Leu Val Val Ser Leu Ser Gln His Pro Ala Glu



130

135

140

Ile Val Ala Ile Ala Glu Ser Gly Lys Thr Lys Pro Lys Pro Arg Asn  
145 150 155 160

Leu Phe His Phe Ile Phe Phe Phe Ile Val Val Leu Leu Ile Asn Cys  
165 170 175

Phe Asn Tyr Asp Asp Phe Gln Leu Phe Phe Asn Lys Leu Ile Phe Ile  
180 185 190

Leu His Phe Leu Leu Tyr Ser Lys  
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Trp Val Arg Lys Tyr  
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<210> 13  
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<400> 13  
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27

<210> 14  
<211> 26  
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<210> 15  
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<210> 17

<211> 22  
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gaacgaaaat ccgaaattat gg 22

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<210> 19  
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<210> 41  
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20 25 30

Gly Lys Ile Ile Arg Ile Phe Asp Asn Ser Phe Val Lys Asp Arg Gln  
35 40 45

Ala Glu Ile Glu Lys Ala Lys Asn Phe Asp Phe Asn Thr Val Leu Leu  
50 55 60

Thr Ala Gly Gly Thr Val Gln Asp Lys Ser Phe Asn Gln Ser Ile Trp  
65 70 75 80

Glu Ala Val Leu Glu His Tyr Asp Gln Ile Glu Lys Thr Thr Asn Leu  
85 90 95

Asp Arg Val Ser Gln Glu Thr Asn Asn Gln Ser Glu Leu Ile Gly Lys  
100 105 110

Tyr Lys Asn Phe Leu Asn Gly Asn Lys Asn Val Trp Ile Leu Thr Gly  
115 120 125

Phe Gln Gln Gly Gln Glu Phe Pro Lys Phe Leu Lys Gln Thr Asp Ser  
130 135 140

Asn Gly Lys Lys Tyr Ser Asp Leu Leu Ala Glu Lys Lys Val Ile Ile  
145 150 155 160

Val Ala Val Asp Trp Asp Leu Ser Lys Glu Asp Lys Asp Leu Ile Lys  
165 170 175

Ala Gly His Phe Ile Ser Leu Leu Tyr Lys Thr Glu Glu Ala Gly Phe  
180 185 190

Ile Ala Gly Tyr Ala Ser Ser Lys Phe Leu Ala Tyr Lys Phe Pro Asn  
195 200 205

Asp Glu Ala Lys Arg Thr Ile Ala Pro Phe Gly Gly Gly His Gly Ala  
210 215 220

Gly Val Thr Asp Phe Ile Ala Gly Phe Leu Ala Gly Ile Ala Lys Tyr  
225 230 235 240

Asn Asn Asp Asn Pro Thr Ala Lys Val Thr Ile Ser Asp Asn Asn Ile  
245 250 255

Asn Ile Asp Thr Gly Phe Ile Ser Asn Asp Lys Thr Ala Thr Phe Ile  
260 265 270

Asn Gly Ile Val Asn Lys Ser Ser Leu Val Leu Pro Val Ala Gly Ser  
275 280 285

Leu Thr Ser Ser Val Val Asp Ala Ile Lys Lys Ser Asn Lys Asp Thr  
290 295 300

Lys Tyr Leu Ile Gly Val Asp Thr Asp Gln Ser Lys Ile Phe Ser Pro  
305 310 315 320

Ala Thr Val Phe Phe Thr Ser Ile Glu Lys His Leu Gly Arg Thr Ile  
325 330 335

Tyr Gln Val Leu Thr Asp Ile Trp Leu Lys Lys Glu Asp Ser Lys Phe  
340 345 350

Leu Gly Ser Phe Arg Ser Phe Lys Leu Thr Asn Pro Ala Asn Ala Thr  
355 360 365

Val Tyr Lys Gly Ile Ser Asp Asp Phe Val Gly Val Ser Asn Ser Thr  
370 375 380

Val Ala Asp Ala Asp Lys Val Lys Ala Gln Glu Phe Leu Asn Glu Ala  
385 390 395 400

Thr Ala Asp Phe Lys Lys Gln Ile Gln Ala Asn Pro Thr Asn Tyr Lys  
405 410 415

Ser Val Leu Gly Ile Pro Thr Met Leu Ile Asn Asp Asn Asp Ala Lys

420

425

430

Asp Asn Glu Lys Ala Ser Leu Phe His Phe Asp Asn Trp Gln Thr Tyr  
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Trp Ala Phe His Ser Arg Phe Ile Asn  
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<213> Artificial Sequence

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Trp Asp Lys Glu

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